

rng-5719

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: January 21, 2007, 23:54:16 ; Search time 41.28 Seconds
(without alignments)
4222.534 Million cell updates/sec

Title: US-10-750-622-5719
Perfect score: 25
Sequence: 1 aacacactgggacatgctcgcatc 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					Description
Result	Query	Match	Length	DB	ID		
No.	Score						
1	19.2	76.8	4141	10	ADE57243		Ade57243 Rat gene
2	17.8	71.2	1524	2	AAV32819		Aav32819 Human dea

071-5719

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OM nucleic - nucleic search, using sw model

Run on: January 21, 2007, 19:04:00 ; Search time 10.76 Seconds
(without alignments)
4347.372 Million cell updates/sec

Title: US-10-750-622-5719
Perfect score: 25
Sequence: 1 aacacactgggacatgctcgcatc 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
c 1	17.8	71.2	601	3	US-09-949-016-28895	Sequence 28895, A
c 2	17.8	71.2	601	3	US-09-949-016-140881	Sequence 140881,
3	17.8	71.2	37622	3	US-09-949-016-12294	Sequence 12294, A
4	17.8	71.2	37622	3	US-09-949-016-15726	Sequence 15726, A
5	17.8	71.2	767677	3	US-09-949-016-12147	Sequence 12147, A
6	17.8	71.2	767677	3	US-09-949-016-17361	Sequence 17361, A
7	17.6	70.4	709	3	US-09-270-767-7641	Sequence 7641, Ap

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OM nucleic - nucleic search, using sw model

Run on: January 21, 2007, 23:54:16 ; Search time 990.72 Seconds
(without alignments)
4222.534 Million cell updates/sec

Title: US-10-750-622-4518
Perfect score: 599.6
Sequence: 1 aaattcttctctctctctct.....cgcagcattaaaagagggcc 600

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					
Result		Query					
No.	Score	Match	Length	DB	ID	Description	
1	50.8	8.5	59446	10	AAD47904	Aad47904 Human tra	
2	50.4	8.4	110000	14	AEE04876_1	Continuation (2 of	

ni-4518

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OM nucleic - nucleic search, using sw model

Run on: January 21, 2007, 19:04:00 ; Search time 258.24 Seconds
(without alignments)
4347.372 Million cell updates/sec

Title: US-10-750-622-4518
Perfect score: 599.6
Sequence: 1 aaattcttctcctcctctct.....cgcagcattaaaagagggcc 600

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%					ID	Description
	No.	Score	Match	Length	DB		
c	1	52.4	8.7	55841	3	US-09-949-016-16602	Sequence 16602, A
	2	50.8	8.5	601	3	US-09-949-016-70771	Sequence 70771, A
	3	50.8	8.5	61462	3	US-09-949-016-17522	Sequence 17522, A
	4	49.6	8.3	106924	3	US-09-949-016-13834	Sequence 13834, A
	5	46.6	7.8	300402	3	US-09-949-016-13632	Sequence 13632, A
c	6	45.2	7.5	670689	3	US-09-949-016-12505	Sequence 12505, A
c	7	45.2	7.5	670690	3	US-09-949-016-14207	Sequence 14207, A